Guest Editor's Forward

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This is the special issue devoted to bioinformatics research in Singapore. Bioinformatics research in Singapore started largely in 1996 when the Bioinformatics Center, National University of Singapore, was formed. With the government's efforts to turn Singapore into a powerhouse of biomedical research, the Genome Institute of Singapore and the Bioinformatics Institute of Singapore have been established since 2000. Recently, a bioinformatics research center was also formed in the Nanyang Technological University. Currently, there are a large number of bioinformatics research teams in each of these institutions.

The biological focuses of the selected papers in this special issue span a very wide range of computational biology and represent several research projects that are undergoing in Singapore:

1. Kong and Han's invited review paper covers the biological and computational perspectives of microRNA, a hot subject in molecular biology and genomics.

2. Li and Leong's paper is about the feature selection for the prediction of translation initiation sites.

3. Wu, Liu, Xu, Peng, and Setiono's paper analyzes the genome-wide gene expression in the Zebrafish genome.

4. Sun, Zhou, and Lin's paper studies the evolution of the RhoGEF-containing protein domains. Kui Lin had worked in the Bioinformatics Center, National University of Singapore, and then in the Genome Institute of Singapore for several years before moving back to Beijing recently.

5. Yao, Xiao, Tung, and Sung's paper investigates the problem of identifying common substructures of proteins.

6. Nguyen, Ngo, and Nguyen's paper studies the genome rearrangement with weighted, length-restricted reversals.

These papers have been subjected to the normal refereeing process and have undergone revision. I am grateful to the authors and especially the referees for making this special issue possible.